SEQUENCE LISTING

<110	> Sele	core	Gmb	Н												
<120>	Metho	d for	the id	dentifi	catior	of e	enzym	nes w	ith de	esired	char	acter	istics	by and	choring t	he reaction
	produ	cts on	the s	urface	of er	nzyme	e-pres	sentin	g org	anism	ıs					
<130	→ Н276	H2768 PCT S3														
<1502 <1512																
<160>	2															
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<210; <211; <212; <213;	2173 DNA	idomo:	nas a	aeruç	ginos	sa.										
<220><221><222><222><223>	CDS (206	5) (2143)												
.400>																•
<400> gaaga	1, agatc	ggcc	tgtg	gg cg	ggtad	ettet	gc!	tgggg	ggtc	gcto	etget	gg t	taata	aatggo	: 6	0
aatga	gcctg	ctgc	gttc	ct co	geega	acaa	a gc	catga	agcc	ggtt	ccg	ege t	tatgo	etgtto	: 12	0
ggctg	aggag	gctt	tacga	ac go	gcc	cggg	ggc	gcato	gccg	acga	ecgco	gc g	ggcc	cgacaa	18	0
taaaa	acaaa	tcat	ggagi	ca aç	jaga			aga Arg	_			_		_	23	2
	cg gco la Ala														28	0
cct t Pro S	eg cco	tat Tyr	tcg Ser 30	acg Thr	ctg Leu	gtg Val	gtg Val	ttc Phe 35	ggc Gly	gac Asp	agc Ser	ctc Leu	agc Ser 40	gat Asp	32	8
	gg cag ly Gln					_					_		-	-	37	6
	hr Asn 60														42	4
Phe G	ga ccg ly Pro														47	2
ccg g	gt gac	ctg	gct	gcc	tcg	acc	tcg	ccg	gtc	aac	gcc	cag	cag	ggc	52	0

												•				
Pro 90	Gly	Asp	Leu	Ala	Ala 95	Ser	Thr	Ser	Pro	Val 100	Asn	Ala	Gln	Gln	Gly 105	•
			ggc Gly													568
			tcg Ser 125													616
			ctg Leu													664
_		_	ggt Gly	_	_	_			_							712
		-	ttt Phe		_		_				_	_	_	Āla		760
			ggt Gly		Leu											808
	_		tac Tyr 205			_		_			-	_		_		856
			ttc Phe													904
			aac Asn													952
aac Asn 250			ccg Pro													1000
aac Asn	ccg Pro	gct Ala	tcc Ser	ttc Phe 270	ggc Gly	ctg Leu	gcc Ala	gcc Ala	gac Asp 275	cag Gln	aac Asn	ctg Leu	atc Ile	ggc Gly 280	acc Thr	1048
tgt Cys	ttc Phe	agc Ser	ggc Gly 285	aac Asn	ggc Gly	tąc Cys	acc Thr	atg Met 290	aac Asn	ccg Pro	acc Thr	tac Tyr	ggg Gly 295	atc Ile	aac Asn	1096
ggc																1144
ccg Pro																1192
ctg	tcg	gcg	ccc	tgg	gag	ctg	acc	ctg	ctg	ccg	gaa	atg	gcc	cac	ggc	1240

Leu 330	Ser	Ala	Pro	Trp	Glu 335	Leu	Thr	Leu	Leu	Pro 340	Glu	Met	Ala	His	Gly 345	
	ctg Leu		-		_		-			_	-		_		_	1288
	gag Glu															1336
	ggc Gly		_	_	_		_			_	_	_	_	_		1384
-	ggc Gly 395					-					-		_		-	1432
	gcc Ala															1480
	gcc Ala															1528
agc Ser	gcc Ala	ttc Phe	gtg Val 445	cag Gln	tac Tyr	cag Gln	gaa Glu	aac Asn 450	cgc Arg	tgg Trp	tgg Trp	gcc Ala	gac Asp 455	gcg Ala	gcg Ala	1576
	acc Thr															1624
	ggc Gly 475															1672
tgg Trp 490	gcg Ala	ttc Phe	agc Ser	gcg Ala	cgc Arg 495	ctg Leu	ggc Gly	tac Tyr	gac Asp	atc Ile 500	gcc Ala	cag Gln	cag Gln	gcc Ala	gac Asp 505	1720
agt Ser	ccc Pro	tgg Trp	cac His	ctg Leu 510	tcg Ser	ccg Pro	ttc Phe	gtc Val	agc Ser 515	Ala	gac Asp	tat Tyr	gca Ala	cgg Arg 520	Val	1768
gag Glu	gtc Val	gac Asp	ggc Gly 525	tat Tyr	tcc Ser	gag Glu	aag Lys	ggc Gly 530	gcc Ala	agc Ser	gcc Ala	acc Thr	gcg Ala 535	ctc Leu	gac Asp	1816
tac Tyr	gac Asp	gac Asp 540	cag Gln	aag Lys	cgc Arg	agc Ser	tcg Ser 545	aag Lys	cgc Arg	ctg Leu	ggc	gcc Ala 550	ggc Gly	ctg Leu	caa Gln	1864
ggc Gly	aag Lys 555	tac Tyr	gcg Ala	ttc Phe	ggc Gly	agc Ser 560	gat Asp	acc Thr	cag Gln	ctg Leu	ttc Phe 565	gcc Ala	gag Glu	tac Tyr	gcc Ala	1912
cac	gaa	cgt	gag	tac	gag	gac	gac	acc	cag	gac	ctg	acc	atg	tcc	ctc	1960

His 570	Glu	Arg	G1u	Tyr	Glu 575	Asp	Asp	Thr	Gln	Asp 580	Leu	Thr	Met	Ser	Leu 585		
		ctg Leu														20	08
_		ctc Leu		_	-					_	_	_	_		_	20	56
		tcg Ser 620														21	04
		cag Gln				-		-	_	_	-		tgaa	aacgo	jcg	21	53
gccg	ggcgd	cc c	gtc	gcgc	ec e											21	73
<210 <211 <212 <213	L> (2> I	? 546 PRT Pseud	lomor	nas a	ierug	jinos	sa										
<400)> 2	2															
Met 1	Ile	Arg	Met	Ala 5	Leu	Lys	Pro	Leu	Val 10	Ala	Ala	Суз	Leu	Leu 15	Ala		
Ser	Leu	Ser	Thr 20	Ala	Pro	Gln	Ala	Ala 25	Pro	Ser	Pro		Ser 30	Thr	Leu		
Val	Val	Phe 35	Gly	Asp	Ser	Leu	Ser 40	Asp	Ala	Gly	Gln	Phe 45	Pro	Asp	Pro		
Ala	Gly 50	Pro	Ala	Gly	Ser	Thr 55	Ser	Arg	Phe	Thr	Asn 60	Arg	Val	Gly	Pro		
Thr 65	Tyr	Gln	Asn	Gly	Ser 70	Gly	Glu	Ile	Phe	Gly 75	Pro	Thr	Ala	Pro	Met 80		
Leu	Leu	Gly	Asn	Gln 85	Leu	Gly	Ile	Ala	Pro 90	Gly	Asp	Leu	Ala	Ala 95	Ser		
Thr	Ser	Pro	Val 100	Asn	Ala	Gln	Gln	Gly 105	Ile	Ala	Asp	Gly	Asn 110	Asn	Trp		
Ala	Val	Gly 115	Gly	Tyr	Arg	Thr	Asp 120	Gln	Ile	Tyr	Asp	Ser 125	Ile	Thr	Ala .		

Ala	Asn	Gly	Ser	Leu	Ile	Glu	Arg	Asp	Asn	Thr	Leu	Leu	Arg	Ser	Arg
	130					135					140				

- Asp Gly Tyr Leu Val Asp Arg Ala Arg Gln Gly Leu Gly Ala Asp Pro 145 150 155 160
- Asn Ala Leu Tyr Tyr Ile Thr Gly Gly Gly Asn Asp Phe Leu Gln Gly
 165 170 175
- Arg Ile Leu Asn Asp Val Gln Ala Gln Gln Ala Ala Gly Arg Leu Val
- Asp Ser Val Gln Ala Leu Gln Gln Ala Gly Ala Arg Tyr Ile Val Val 195 200 205
- Trp Leu Leu Pro Asp Leu Gly Leu Thr Pro Ala Thr Phe Gly Gly Pro 210 215 220
- Leu Gln Pro Phe Ala Ser Gln Leu Ser Gly Thr Phe Asn Ala Glu Leu 225 230 235
- Thr Ala Gln Leu Ser Gln Ala Gly Ala Asn Val Ile Pro Leu Asn Ile 245 250 255
- Pro Leu Leu Lys Glu Gly Met Ala Asn Pro Ala Ser Phe Gly Leu 260 265 270
- Ala Ala Asp Gln Asn Leu Ile Gly Thr Cys Phe Ser Gly Asn Gly Cys 275 280 285
- Thr Met Asn Pro Thr Tyr Gly Ile Asn Gly Ser Thr Pro Asp Pro Ser 290 295 300
- Lys Leu Leu Phe Asn Asp Ser Val His Pro Thr Ile Thr Gly Gln Arg 305 310 315 320
- Leu Ile Ala Asp Tyr Thr Tyr Ser Leu Leu Ser Ala Pro Trp Glu Leu 325 330 335
- Thr Leu Leu Pro Glu Met Ala His Gly Thr Leu Arg Ala Tyr Gln Asp 340 345 350
- Glu Leu Arg Ser Gln Trp Gln Ala Asp Trp Glu Asn Trp Gln Asn Val 355 360 365

G1y	Gln	Trp	Arg	Gly	Phe	Val	Gly	Gly	Gly	Gly	Gln	Arg	Leu	Asp	Phe
	370					375					380				

- Asp Ser Gln Asp Ser Ala Ala Ser Gly Asp Gly Asn Gly Tyr Asn Leu 385 390 395 400
- Thr Leu Gly Gly Ser Tyr Arg Ile Asp Glu Ala Trp Arg Ala Gly Val 405 410 415
- Ala Ala Gly Phe Tyr Arg Gln Lys Leu Glu Ala Gly Ala Lys Asp Ser 420 430
- Asp Tyr Arg Met Asn Ser Tyr Met Ala Ser Ala Phe Val Gln Tyr Gln 435 440 445
- Glu Asn Arg Trp Trp Ala Asp Ala Ala Leu Thr Gly Gly Tyr Leu Asp 450 455 460
- Tyr Asp Asp Leu Lys Arg Lys Phe Ala Leu Gly Gly Glu Arg Ser 465 470 475 480
- Glu Lys Gly Asp Thr Asn Gly His Leu Trp Ala Phe Ser Ala Arg Leu 485 490 495
- Gly Tyr Asp Ile Ala Gln Gln Ala Asp Ser Pro Trp His Leu Ser Pro 500 505 510
- Phe Val Ser Ala Asp Tyr Ala Arg Val Glu Val Asp Gly Tyr Ser Glu 515 520 525
- Lys Gly Ala Ser Ala Thr Ala Leu Asp Tyr Asp Asp Gln Lys Arg Ser 530 540
- Ser Lys Arg Leu Gly Ala Gly Leu Gln Gly Lys Tyr Ala Phe Gly Ser 545 550 555 560
- Asp Thr Gln Leu Phe Ala Glu Tyr Ala His Glu Arg Glu Tyr Glu Asp 565 570 575
- Asp Thr Gln Asp Leu Thr Met Ser Leu Asn Ser Leu Pro Gly Asn Arg 580 585 590
- Phe Thr Leu Glu Gly Tyr Thr Pro Gln Asp His Leu Asn Arg Val Ser 595 600 605

Leu Gly Phe Ser Gln Lys Leu Ala Pro Glu Leu Ser Leu Arg Gly Gly 610 615 620

Tyr Asn Trp Arg Lys Gly Glu Asp Asp Thr Gln Gln Ser Val Ser Leu 625 630 635 640

Ala Leu Ser Leu Asp Phe 645